

ATGACCGCTATGAGCACTGCAATTACACGCCAGATCGTTCTCGATACCGAAACCACCGGTATGAACCAGA 70

mutD
M T A M S T A I T R Q I V L D T E T T G M N Q
TTGGTGCGCACTATGAAGGCCACAAGATCATTGAGATTGGTGCCGTTGAAGTGGTGAACCGTCGCCTGAC 140

mutD
I G A H Y E G H K I I E I G A V E V V N R R L T
GGGCAATAACTTCCATGTTTATCTCAAACCCGATCGGCTGGTGGATCCGGAAGCCTTTGGCGTACATGGT 210

mutD
G N N F H V Y L K P D R L V D P E A F G V H G
ATTGCCGATGAATTTTGTCTGATAAGCCCACGTTTGCCGAAGTAGCCGATGAGTTCATGGACTATATTC 280

mutD
I A D E F L L D K P T F A E V A D E F M D Y I
CGGGCGCGGAGTTGGTGATCCATAACGCAGCGTTCGATATCGGCTTTATGGACTACGAGTTTTCGTTGCT 350

mutD
R G A E L V I H N A A F D I G F M D Y E F S L L
TAAGCGCGATATTCCGAAGACCAATACTTTCTGTAAGGTCACCGATAGCCTTGCGGTGGCGAGGAAAATG 420

mutD
K R D I P K T N T F C K V T D S L A V A R K M
TTTCCCGTAAGCGCAACAGCCTCGATGCGTTATGTGCTCGCTACGAAATAGATAACAGTAAACGAACGC 490

mutD
F P G K R N S L D A L C A R Y E I D N S K R T
TGCACGGGGCATTACTCGATGCCCAGATCCTTGCGGAAGTTTATCTGGCGATGACCGGTGGTCAAACGTC 560

mutD
L H G A L L D A Q I L A E V Y L A M T G G Q T S
GATGGCTTTTGGCGATGGAAGGAGAGACACAACAGCAACAAGGTGAAGCAACAATTCAGCGCATTGTACGT 630

mutD
M A F A M E G E T Q Q Q Q G E A T I Q R I V R
CAGGCAAGTAAGTTACGCGTTGTTTTGCGACAGATGAAGAGATTGCAGCTCATGAAGCCCCTCTCGATC 700

mutD
Q A S K L R V V F A T D E E I A A H E A R L D
TGGTGACAGAAGAAAGGCCGAAGTTGCCTCTGGCGAGCATAA 741

mutD
L V Q K K G G S C L W R A .

FIGURE 1

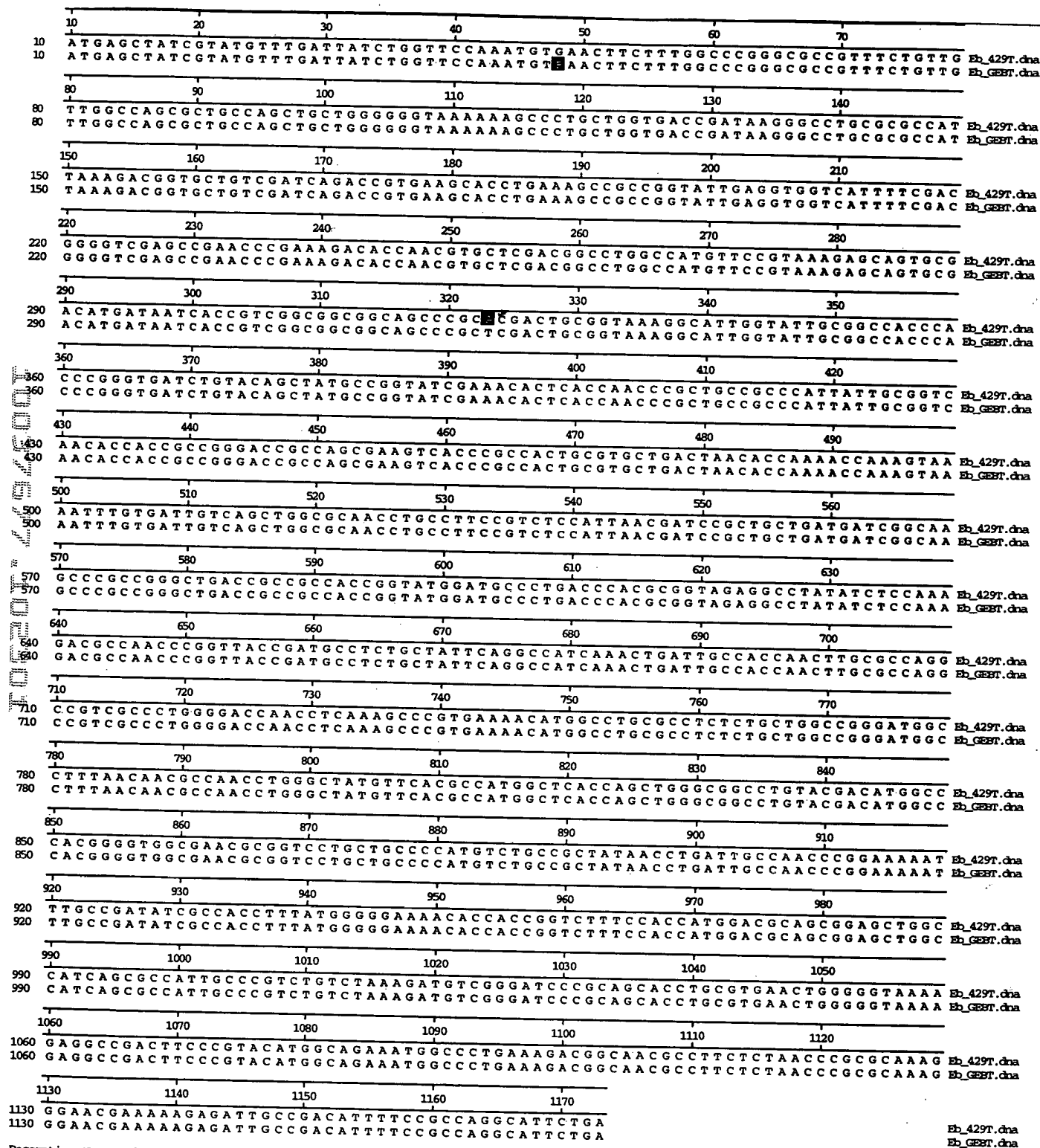
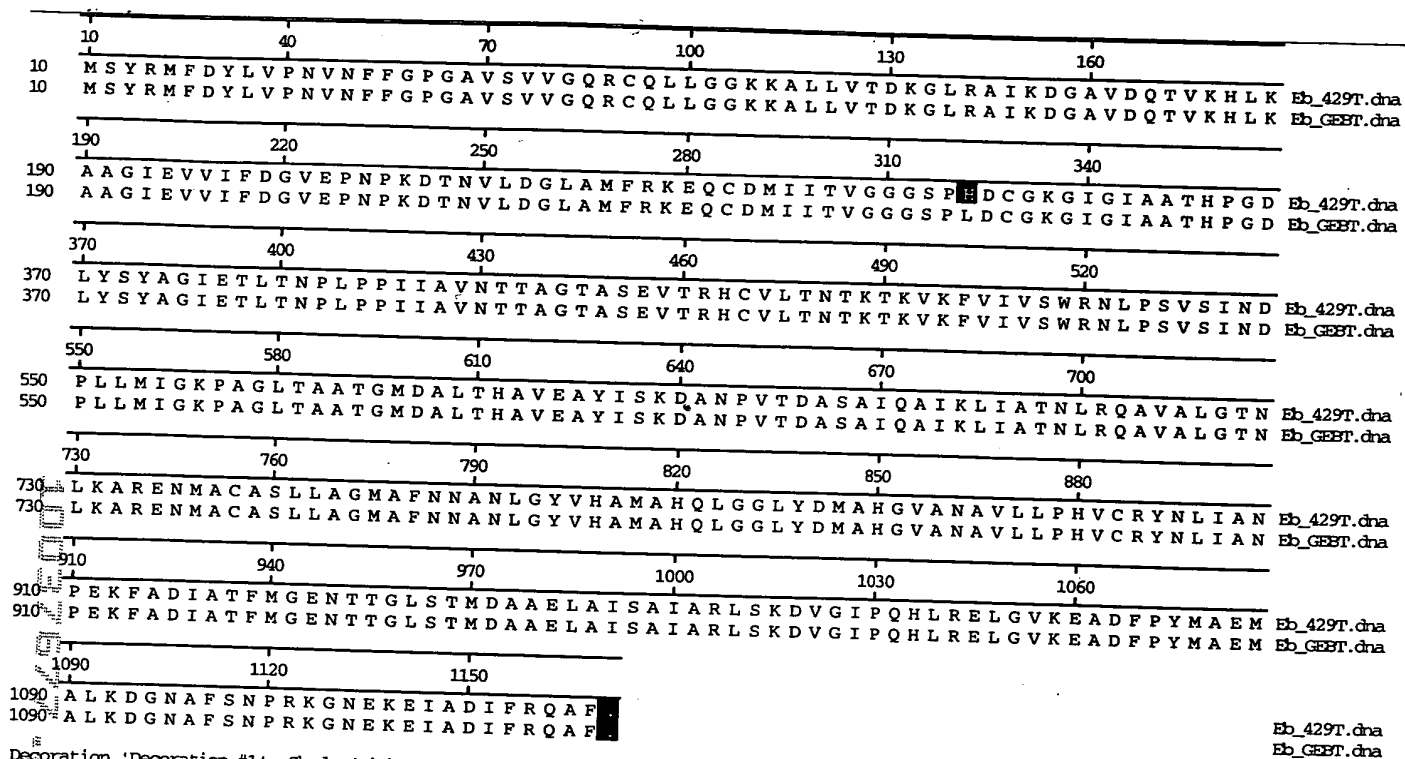


FIGURE 2



10037677-10301

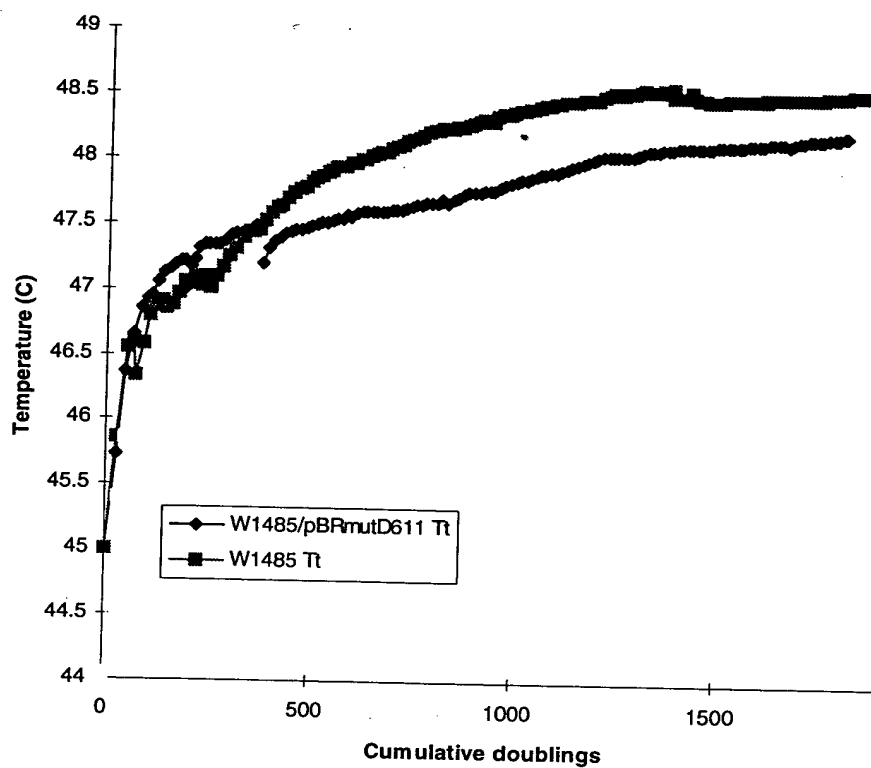


Figure 4

10037677.40301

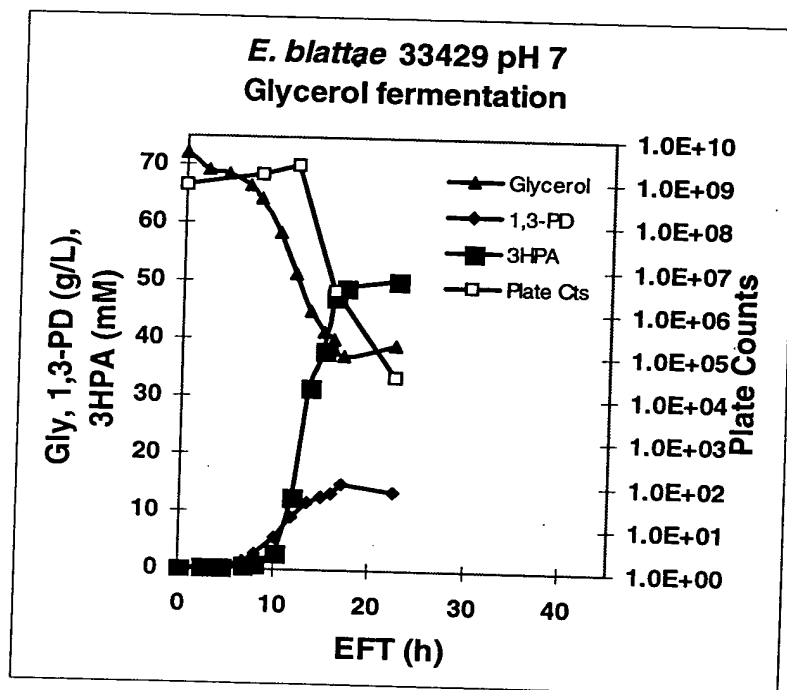


Figure 5

FOE20T* 2/29/2001

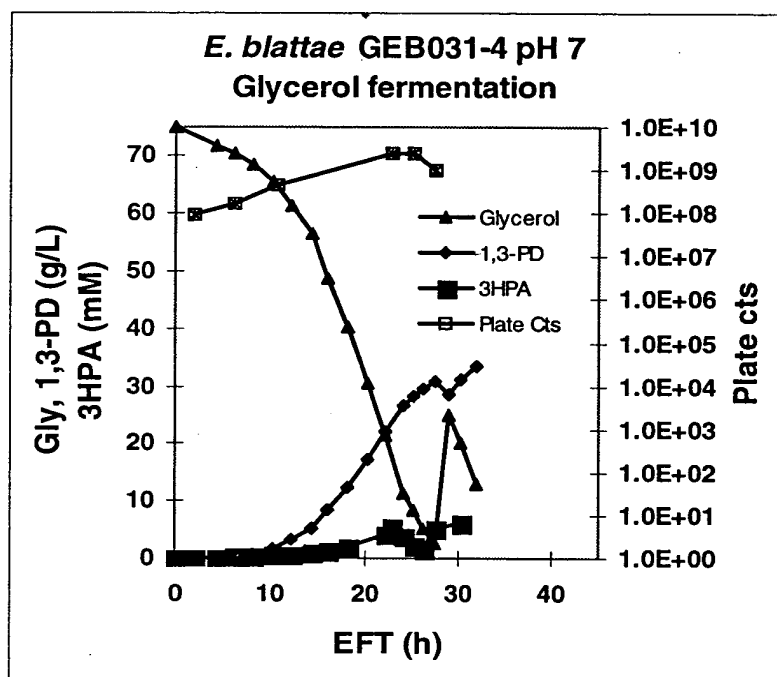


Figure 6